

W098/18930 SEQ ID 66

Query Match
Best Local Similarity 80.9%; Score 575.5; DB 4; Length 763;
Matches 103; Conservative 18; Mismatches 9; Indels 1; Gaps 1;
7 CAYALNQHRS-GENKDNRRVSYVDGSSQSKSENLTTPDQVSOKEGIAEQIIVIKITDQGY 65
1 CSYELGRHQAQGVKKESNRVSYIDGDDAAGOKAENLTPDEVSKREGINAEQXVIRIKITDQGY 60
66 VTSHGDDHYHYNGKVPYDALFSEELLTKKDPNYQLKADADIVNEVGKGYIIKIVDGGKYYVYLK 125
61 VTSHGDDHYHYNGKVPYDALFSEELLTKKDPNYQLKADADIVNEVGKGYIIKIVDGGKYYVYLK 120
126 DAHADNVRTK 136
121 DAHADNVRTK 131

W098/18930 SEQ ID 56

Query Match
Best Local Similarity 80.7%; Score 574; DB 4; Length 796;
Matches 104; Conservative 16; Mismatches 9; Indels 0; Gaps 0;
8 AYALNQHRSQENKDNRRVSYVDGSSQSKSENLTTPDQVSOKEGIAEQIIVIKITDQGYVT 67
1 SYELGLYQARTVKENNRVSYIDGKQATQKTENTLTPDEVSKREGINAEQIIVIKITDQGYVT 60
68 SHGDDHYHYNGKVPYDALFSEELLTKKDPNYQLKADADIVNEVGKGYIIKIVDGGKYYVYLKDA 127
61 SHGDDHYHYNGKVPYDALFSEELLTKKDPNYQLKADADIVNEVGKGYIIKIVDGGKYYVYLKDA 120
128 AHADNVRTK 136
121 AHADNVRTK 129

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7 CAYALNQHRS-GENKDNRRVSVYVDGSSSSQKSENLTTPDOVSQKREGIOAEQIVIKITIDGVT 65
1 SYELGRLYQARTVKENNNRVSIIIDGKQATQKTENLTTPDEVSKREGINAEQIVIKITIDGVT 60
66 VTSHGDDHYHYNGKVPYDALFSEELTMKDPNYQLKADADIVNEVKGGYIIKVDGKYYVYLK 125
61 VTSHGDDHYHYNGKVPYDALFSEELTMKDPNYQLKADADIVNEVKGGYIIKVDGKYYVYLK 120
126 DAHADNVRTK 136
121 DAHADNVRTK 131

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1 SYELGRLYQARTVKENNNRVSIIIDGKQATQKTENLTTPDEVSKREGINAEQIVIKITIDGVT 60
68 SHGDHYHYHYNGKVPYDALFSEELTMKDPNYQLKADADIVNEVKGGYIIKVDGKYYVYLK 127
61 SHGDHYHYHYNGKVPYDALFSEELTMKDPNYQLKADADIVNEVKGGYIIKVDGKYYVYLK 120
128 AHADNVRTK 136
121 AHADNVRTK 129

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